

## SEARCH REQUEST FORM

Requestor's Name: \_\_\_\_\_ Serial Number: \_\_\_\_\_  
Date: \_\_\_\_\_ Phone: \_\_\_\_\_ Art Unit: \_\_\_\_\_

### Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

### STAFF USE ONLY

Date completed: 05/21/82  
Searcher: DAVID G. FORD  
Terminal time: 2:00  
Elapsed time: \_\_\_\_\_  
CPU time: \_\_\_\_\_  
Total time: 2:30  
Number of Searches: \_\_\_\_\_  
Number of Databases: 1

**Search Site**  
\_\_\_\_ STIC  
\_\_\_\_ CM-1  
\_\_\_\_ Pre-S  
**Type of Search**  
\_\_\_\_ N.A. Sequence  
\_\_\_\_ A.A. Sequence  
\_\_\_\_ Structure  
\_\_\_\_ Bibliographic

**Vendors**  
\_\_\_\_ IG  
\_\_\_\_ STN  
\_\_\_\_ Dialog  
\_\_\_\_ APS  
\_\_\_\_ Geninfo  
\_\_\_\_ SDC  
\_\_\_\_ DARC/Questel  
\_\_\_\_ Other CGA



Result No.	Score	Query Match	Length	ID	Description
1	1447	100.0	347	AA113369	Acetic acid sequence
2	1347	100.0	347	AA080217	Human PR-223 gene
3	1343	99.8	347	AA068200	Human sorcin gene
4	1339	99.6	347	AA064537	Human liver cell c
5	721	37.0	1785	AA064591	Human SRCR protein
6	719	36.9	422	AA039416	Human 3-11-94-20FF
7	695	35.7	552	AA039417	Human 3-11-94-20ER
8	691.5	35.5	1453	AA066037	Human TAF9-234
9	690	35.4	1319	AA066040	Human TAF9-234
10	686	35.4	1413	AA066039	Human TAF9-234 ma
11	686	35.2	1321	AA039414	Human 3-11-94-20

## ADMINISTRATIVE

17-SEP-1997; 0000-0009122;  
17-SEP-1997; 0000-0009184;  
17-SEP-1997; 0000-0009184;

Human polyprotein
Human polyprotein
Human polyprotein
Human secreted protein
Human full-length protein W61 protein
Human serine protease
Human neurotrophin
Mouse serine protease
Mouse neural lysin
Human Elastin S1
Human C153 or C5
Human liver cell p
Human liver oxidas
Anthrax toxin sequence
Clone H0HC84 #1
Human SHCR protein
Human secreted protein
Human C153 or C5
Human C153 or C5
Human lipid metabo
Human lysoz oxidas
Human lysoz oxidas
Proteinase subtilis
Trypsin-like enzyme
Human secreted pro
Peptide fragment n
Protein fragment n
Gene 15 human sequ
Human protein sequ
Human protein sequ
A cathepsin like c
Human cathepsin l
Secreted human lung











[illegible]

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14-JUN-1999: 9405-0343159.
XX
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX McCarthy SA, Fraser CC, Sharp JD, Barnes TM;
XX
XX WPI: 2001-032314704.
XX
XX TANGO and INTERCEPT nucleic acids, proteins, and antibodies, useful for
XX screening assays and diagnostic assays and for the treatment of
XX neurological diseases such as Alzheimer's, Parkinson's and Huntington's
XX disease -
XX
XX Claim 8; Pages 261-287; 65pp; English.
XX
XX The present invention relates to TANGO and INTERCEPT proteins and coding
XX sequences (see AA45121-45136 and AA45139-45179 and AA462931-966597,
XX AA866084-B66083 and AA866085); the TANGO/INTERCEPT proteins and coding
XX sequences are useful for the treatment of neurological disorders such as
XX central nervous system (CNS) disorders, CNS-related disorders, focal
XX brain disorders, global/diffuse cerebral disorders and other
XX neurological and cerebrovascular disorders; the CNS disorders include
XX Alzheimer's disease, senile dementia, Huntington's disease, amyotrophic
XX lateral sclerosis, Parkinson's, Gilles de la Tourette's Syndrome,
XX autonomic function disorders such as hypertension and sleep disorders,
XX cerebrovascular disorders, psychiatric substance use disorders,
XX anxiety, and bipolar affective disorder.
XX
XX Sequence 1319 AA;
XX
XX 2003 Match 3-19, Score 599, E-62; Length 1419;
XX Best Local Similarity 42.5%; Prod. No. 1-86-48;
XX Matches 139, Substitutions 39, Mismatches 119, Indels 15, Gaps 69
XX
XX 24 VLVGSGHGRCELEVLVLEQWGVVGVGVWVLEIVAVVLEKSLGAGAGVGLVLYEPVA 83
XX IIII I IIII IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
XX 8 LIIIVGPIGSGTGVKIIIVGIVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGV 64
XX IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
XX 34 IFLKAVIIEGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGV 141
XX IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
XX 37 IIVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGV 118
XX IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
XX 143 IIVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGV 201
XX IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
XX 119 KLVGSGHGRCELEVLVLEQWGVVGVGVWVLEIVAVVLEKSLGAGAGVGLVLYEPVA 177
XX IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
XX 202 KLVGSGHGRCELEVLVLEQWGVVGVGVWVLEIVAVVLEKSLGAGAGVGLVLYEPVA 159
XX IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
XX 178 KLVGSGHGRCELEVLVLEQWGVVGVGVWVLEIVAVVLEKSLGAGAGVGLVLYEPVA 237
XX IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
XX 200 KLVGSGHGRCELEVLVLEQWGVVGVGVWVLEIVAVVLEKSLGAGAGVGLVLYEPVA 219
XX IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
XX 238 KLVGSGHGRCELEVLVLEQWGVVGVGVWVLEIVAVVLEKSLGAGAGVGLVLYEPVA 295
XX IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
XX 320 VLVGSGHGRCELEVLVLEQWGVVGVGVWVLEIVAVVLEKSLGAGAGVGLVLYEPVA 346
XX IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
XX 296 KLVGSGHGRCELEVLVLEQWGVVGVGVWVLEIVAVVLEKSLGAGAGVGLVLYEPVA 322
XX IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
XX
XX RESULT 10
XX AA866039
XX ID: AA866039 standard; Protein: 1413 AA.
XX
XX AA866049;
XX
XX 30 MAR 2001 (first entry)
XX
XX Human TANGO 234 mature protein.
XX
XX TANGO protein, INTERCEPT protein; neurological disorder;
XX central nervous system; focal brain disorder; bipolar affective disorder;
XX global diffuse cerebral disorder; cerebrovascular; Alzheimer's disease;

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KW	Senile dementia; Huntington's disease; amyotrophic lateral sclerosis; Parkinson's; Gilles de la Tourette's syndrome; hyperkinesia; sleep; neuropsychiatric; psychoactive substance use; anxiety.
CS	Bromo sapiens.
XX	
FN	W0200077499 A2.
FD	24 DEC 2000.
FD	24 MAY 2001; 24 NOV 2001.
FD	14 JUN 1999; 9405 034319.
FA	(MILL.) MILLENNIUM PHARM INC.
FI	McCarthy SA, Fraser CV, Sharp JD, Barnes TM;
XX	
DP	WPI: 2001-032419/04.
XX	
PT	TANQ and INHREPT nucleic acids, proteins, and antibodies, useful for screening assays and diagnostic assays and for the treatment of neurological diseases such as Alzheimer's, Parkinson's and Huntington's disease.
XX	
PS	Claim 45: Pages 276-281; 59pp; English.
XX	
CC	The present invention relates to TANQ or INHREPT 12-oligo and 3'-oligo sequences (see: AAF45121, F45136 and AAF45138, F45139 and AAF46057, AAF66064, AAF6093 and AAF6095). The TANQ/INHREPT proteins and coding sequences are useful for the treatment of neurological disorders such as central nervous system (CNS) disorders. CNS related disorders such as brain disorders, global diffuse cerebral disorders and other neurological and cerebrovascular disorders. The CNS disorders include Alzheimer's disease, senile dementia, Huntington's disease, amyotrophic lateral sclerosis, Parkinson's, Gilles de la Tourette's syndrome, autonomic function disorders such as hypertension and sleep disorders, neuropsychiatric disorders, psychiatric substance use disorders, anxiety, and bipolar affective disorder.
XX	
SL	Sequence 1413 AA

[illegible]

AA	AM9493
ID	AAM39493 standard; Protein: 1121 AA.
XX	
AC	AAM39493;
XX	
BT	22-JUL-2001 (first entry)
XX	
DE	Human polypeptide SEQ ID NO 2638.
XX	
KW	Human; neuropathic immunosuppressive cytototoxic role therapy; cancer; peripheral nervous system; neuropathy; central nervous system; Alz-
BW	Alzheimer's; Parkinson's disease; inflammation; Scleroderma; laboredative; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic drug screening; arthritis; inflammation; leukaemia.
KW	
XX	
OS	Homo sapiens.
XX	
PN	WO200153312-A1.
XX	
PP	26-JUL-2001.
XX	
FF	26 JUL 2000 2000A02 4763.
XX	
IR	21-JAN-2000; 2000US 0498725. 25-APR-2000; 2000US-0552317. 09-JUL-2000; 2000US-0598042. 19 SEP 2000 2000S 0628712. 03 AUG 2000 2000US 0653450. 14 SEP 2000 2000US-0662191. 19-OCT-2000; 2000US-0694046. 29 NOV 2000; 2000US 0727344.
XX	
FA	(HVSF)- HVSFQ INC.
XX	
P1	Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
E1	Guan J, Wang Z, Wehrung L, Xu C, Xue AJ, Yang Y, Zhang J;
E4	Zhao QA, Zhou P, Goodrich R, Demande RT;
XX	
RK	WP1: 2001 44257/47.
RK	N-PSDB: AAI58649.
XX	
PT	Novel nucleic acids and polypeptides, useful for treatment disorders such as central nervous system injuries
XX	
PS	Example 4; SEQ ID NO 2638; 10078pp; English.
XX	
VC	The invention relates to human nucleic acids (AAI57998-AAI61469) and the encoded polypeptides (AAM38642-AAM42214) with neurotropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localized neurogathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, multiple sclerosis, stroke, motor neuron disease, the utilization of the activities such as: immune system suppression, Alzheimer's disease, stroke, multiple sclerosis, myopathy, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, neurological activity, utilization of polymers, leukocytes and C.N.S disorders.
CC	Note: The sequence data for this patent did not form part of the printed specification.
XX	
Sequence	1121 AA:

```
Query Match      30.2%   Score 686; 148 22; Length 1121;
Best Local Similarity    39.1%; Prod. No. 4-20-448;
Matches 147; Conserved Ite 55; Mismatches 142; Indels 26; Gaps 8;
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Genware version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM Protein protein search, using sw model

Run on: August 20, 2002, 12:57:45, Search time 11:07 seconds  
(with hour alignments)  
648,484 Million cell updates/Gs

Title: US-09-904-462A-148

Perfect score: 1947

Sequence: 1 MALPESLILACTRCEFLAS.....KFWHEDLHGMWAVDSV 47

Scoring table: PloSUM-2

Gapop 10.0, Gapext 0.5

Searched: 231628 seqs, 2445594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Issued\_Patents\_AA:\*

1: 10025 11 1014 2 10025AA 2000-09-16  
2: 10025 11 1014 2 10025AA 2000-09-16  
3: 10025 11 1014 2 10025AA 2000-09-16  
4: 10025 11 1014 2 10025AA 2000-09-16  
5: 10025 11 1014 2 10025AA 2000-09-16  
6: 10025 11 1014 2 10025AA 2000-09-16

Pred. NC is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1928	99.5	346	US-09-034-916-2	Sequence 2, Appl
2	721	37.0	1785	US-09-341-587-3	Sequence 3, Appl
3	588	23.2	181	US-09-034-916-4	Sequence 4, Appl
4	585	30.1	102	US-09-034-916-5	Sequence 5, Appl
5	582.5	29.9	1290	US-08-478-795-2	Sequence 6, Appl
6	553	28.4	101	US-09-034-916-3	Sequence 3, Appl
7	480	24.7	753	US-09-276-400-2	Sequence 2, Appl
8	480	24.7	753	US-09-448-676-2	Sequence 2, Appl
9	475	24.4	466	US-09-341-587-1	Sequence 1, Appl
10	463.5	23.8	754	US-09-276-400-8	Sequence 8, Appl
11	463.5	23.8	754	US-09-418-076-8	Sequence 8, Appl
12	453.5	22.3	774	US-09-276-400-7	Sequence 7, Appl
13	453.5	22.3	774	US-09-448-676-7	Sequence 7, Appl
14	285	14.6	100	US-06-034-916-15	Sequence 15, Appl
15	282	14.5	100	US-06-034-916-1	Sequence 1, Appl
16	279	14.3	100	US-09-034-916-10	Sequence 10, Appl
17	276	13.7	100	US-03-034-916-11	Sequence 11, Appl
18	260.5	13.4	495	US-08-794-795-2	Sequence 2, Appl
19	260.5	13.4	495	US-09-249-200-2	Sequence 2, Appl
20	260.5	13.4	520	US-08-794-795-6	Sequence 6, Appl
21	250.5	13.4	520	US-09-249-200-6	Sequence 6, Appl
22	258.5	13.3	451	US-08-154-365-2	Sequence 2, Appl
23	254.5	13.1	101	US-09-034-916-9	Sequence 9, Appl
24	252.5	13.0	451	US-08-453-117-2	Sequence 2, Appl
25	252.5	13.0	451	US-08-918-222-2	Sequence 2, Appl
26	252.5	13.0	451	US-08-973-145-2	Sequence 2, Appl
27	252.5	13.0	451	US-09-276-400-10	Sequence 10, Appl

28 252.5 13.0 451 4 US-09-448-676-10  
29 252.5 13.0 451 5 US-09-448-676-10  
30 251 12.9 101 4 US-09-518-046-15  
31 247.5 12.7 489 2 US-08-794-795-7  
32 247.5 12.7 489 4 US-09-249-200-7  
33 247.5 12.7 518 1 US-08-392-367B-2  
34 247.5 12.7 518 3 US-08-893-467A-2  
35 247 12.7 101 4 US-09-518-046-16  
36 246 12.6 453 6 US-04-666-4  
37 229.5 11.8 55 3 US-09-034-916-7  
38 216 11.1 585 1 US-08-477-674-10  
39 216 11.1 585 1 US-08-477-674-10  
40 216 11.1 585 2 US-08-316-791-10  
41 216 11.1 585 3 US-08-473-673-10  
42 207 10.6 100 3 US-09-034-916-13  
43 205.5 10.6 100 3 US-09-034-916-12  
44 193.5 9.9 349 3 US-08-630-172-6  
45 193.5 9.9 349 4 US-09-375-419-6

ALIGNMENTS

RESULT 1  
US-09-034-916-2  
Sequence 2, Application US/09034916  
Patent No. 6046314

GENERAL INFORMATION:  
APPLICANT: GEBE, JOHN A.

APPLICANT: STADAK, ANTHONY W.

ATTORNEY: ARSLOV, ALEXANDRO A.

INVENTOR: R. STADAK, A. WELLS, J. VERDE, R. RECEPTOR

INVENTOR: STADAK, ANTHONY W.

INVENTOR: STADAK, ANTHONY W.

INVENTOR: STADAK, ANTHONY W.

INVENTOR: STADAK, ANTHONY W.

INVENTOR: STADAK, ANTHONY W.

ADDRESS: ROBINS & ASSOCIATES

STREET: 50 MIDDLEFIELD ROAD, SUITE 200

CITY: MENLO PARK

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94025

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: 09/034,916

FILING DATE: 04-MAR-1998

CLASSIFICATION: 535

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/049,956

FILING DATE: 06-MAR-1997

ATTORNEY/AGENT INFORMATION:

NAME: ROBINS, ROBERTA L.

REGISTRATION NUMBER: 33,208

REFERENCE CIT NUMBER: 59-48-0220

TELECOMMUNICATION INFORMATION:

TELEPHONE: (450) 325-7812

TELEFAX: (450) 325-7823

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 346 amino acids

TYPE: amino acid

TOPOLOGY: Linear

MOLECULE TYPE: protein

US-09-034-916-2

Query Match: 99.5%, Score: 1928, DB ID: Length: 346;

Best local Similarity: 100.0%; Pred. No.: 276-177;

Motifs: 345, Conservative: 0, Mismatches: 0, Gaps: 0;





[illegible]

RESULT 8  
US-04-443-076-2

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US-09-448-076-2
: Sequence 2, Application US/00448076
: Patent No. 6300092
: GENERAL INFORMATION:
: APPLICANT : Rhodadoust, Mohjan et al.
: TITLE OF INVENTION: METHODS OF USE OF A NOVEL LYSYL OXIDASE RELATED PROTEIN
: FILE REFERENCE: MNL 0730P
: CURRENT APPLICATION NUMBER: US-09-448-076
: CURRENT FILING DATE: 1999-11-24
: EARLIER APPLICATION NUMBER: 60/117,580
: EARLIER FILING DATE: 1996-01-27
: EARLIER APPLICATION NUMBER: 09/276,400
: EARLIER FILING DATE: 1998-08-25
: NUMBER OF SEQ ID NOS: 12
: SOFTWARE: Patent In Ver. 2.0
: SEQ ID NO 2
: LENGTH: 753
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-448-076-2

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James M. Smith

[illegible]

Matches	129.	Conservative	57.	Mismatches	145.	Indels	78.	Gaps	13.
Base pair similarity	91.6.	LOC100	140.		177.				

[illegible]
$$\{V_1, V_2, V_3, V_4, V_5, V_6, V_7, V_8, V_9, V_{10}, V_{11}, V_{12}, V_{13}, V_{14}, V_{15}, V_{16}, V_{17}, V_{18}, V_{19}, V_{20}, V_{21}, V_{22}, V_{23}, V_{24}, V_{25}, V_{26}, V_{27}, V_{28}, V_{29}, V_{30}, V_{31}, V_{32}, V_{33}, V_{34}, V_{35}, V_{36}, V_{37}, V_{38}, V_{39}, V_{40}, V_{41}, V_{42}, V_{43}, V_{44}, V_{45}, V_{46}, V_{47}, V_{48}, V_{49}, V_{50}, V_{51}, V_{52}, V_{53}, V_{54}, V_{55}, V_{56}, V_{57}, V_{58}, V_{59}, V_{60}, V_{61}, V_{62}, V_{63}, V_{64}, V_{65}, V_{66}, V_{67}, V_{68}, V_{69}, V_{70}, V_{71}, V_{72}, V_{73}, V_{74}, V_{75}, V_{76}, V_{77}, V_{78}, V_{79}, V_{80}, V_{81}, V_{82}, V_{83}, V_{84}, V_{85}, V_{86}, V_{87}, V_{88}, V_{89}, V_{90}, V_{91}, V_{92}, V_{93}, V_{94}, V_{95}, V_{96}, V_{97}, V_{98}, V_{99}, V_{100}\}$$
[illegible][illegible]

1. *Chlorophyll a* (Chl *a*) is the primary photosynthetic pigment in most plants and algae. It is a green pigment that absorbs light energy in the blue and red regions of the visible spectrum. Chl *a* is essential for the light-dependent reactions of photosynthesis, where it converts light energy into chemical energy.

2. *Chlorophyll b* (Chl *b*) is an accessory pigment found in green plants and algae. It is a yellow-green pigment that absorbs light energy in the blue and orange regions of the visible spectrum. Chl *b* transfers the absorbed energy to Chl *a* for use in photosynthesis.

3. *Carotenoids* are a group of pigments that include carotenes and xanthophylls. They are responsible for the yellow, orange, and red colors seen in autumn foliage. Carotenoids absorb light energy in the blue and green regions of the visible spectrum and transfer the energy to Chl *a*. They also play a role in protecting the photosynthetic apparatus from damage by excess light energy.

4. *Xanthophylls* are a subset of carotenoids that are responsible for the yellow color of autumn leaves. They absorb light energy in the blue and green regions of the visible spectrum and transfer the energy to Chl *a*. Xanthophylls also play a role in protecting the photosynthetic apparatus from damage by excess light energy.

5. *Anthocyanins* are water-soluble pigments that are responsible for the red, purple, and blue colors seen in autumn foliage. They are not involved in photosynthesis but are produced by the plant in response to environmental factors such as low temperatures and high light intensity.

# THE UNIVERSITY OF CHICAGO

[illegible]

INDEX OF ASTRONOMICAL OBSERVATIONS

|| VYB, SHUBA, ASEN - PESSYVE, (VRYAL) FIF - KRV: PZ

131 N5DCTHDEHAGVICKDQKLGTFSDSNVIFVEHHIQVEVKIRFPAVCGWCKRFLIVFELVE 160

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191 VRLPQWSSQVCLKQWSAHSNHSIVVSTMLG 115EKRVNAATYKLLAQKGLHSHG - 242

852 J. HAMPEL, L. N. MATHIAS and C. A. VERGOS

[illegible]

243 - LHEVACV;EEAHLSTLSLEHYRANI;ALGTPQ;H;H;AVVS;V;D;H;V;A;A;S;V;K;K;A;A;S;K;K) 501

[REDACTED]





```

1  NUMBER OF SEQUENCES: 17
2  CORRESPONDENCE ADDRESS:
3  ADDRESSEE: ROBINS & ASSOCIATES
4  STREET: 90 MIDDLEFIELD ROAD, SUITE 200
5  CITY: MENLO PARK
6  STATE: CALIFORNIA
7  COUNTRY: USA
8  ZIP: 94025
9  COMPUTER READABLE FORM:
10 MEDIUM TYPE: Floppy disk
11 COMPUTER: IBM PC compatible
12 OPERATING SYSTEM: PC-DOS/MS-DOS
13 SOFTWARE: Patent In Release #1.0, Version #1.30
14 CURRENT APPLICATION DATA:
15 APPLICATION NUMBER: US/09-034-916
16 FILING DATE: 04-MAR-1998
17 CLASSIFICATION: 536
18 PRIOR APPLICATION DATA:
19 APPLICATION NUMBER: US 60/039,956
20 FILING DATE: 06-MAR-1997
21 ATTORNEY/AGENT INFORMATION:
22 NAME: ROBINS, ROBERTA L.
23 REGISTRATION NUMBER: 34,208
24 REFERENCE/EX-REF NUMBER: 5998-0020
25 TELECOMMUNICATION INFORMATION:
26 TELEPHONE: (650) 325-7812
27 TELEFAX: (650) 325-7823
28 INFORMATION FOR SEQ ID NO: 15:
29 SEQUENCE CHARACTERISTICS:
30 LENGTH: 100 amino acids
31 TYPE: amino acid
32 STRANDEDNESS: single
33 TOPOLOGY: linear
34 MOLECULE TYPE: DNA (genomic)
35 US-09-034-916-15

Query Match 14.5%, Score 282; DB 3; Length 100;
Best Local Similarity 50.0%; Pred. No. 20;
Matches 51; Conservative 17; Mismatches 32; Gaps 2;

QY 245 RLVGRLNLSGSELEVLHKGVMWSVTHRWWEDEALQVYVCHLEDSHSESEPEHKLGYGPG 304
DB 1 RLVGRLNLSGSELEVLHKGVMWSVTHRWWEDEALQVYVCHLEDSHSESEPEHKLGYGPG 304

QY 305 VPRITDNYVRCSGEESQSFQCHRFWGFHDCIHQEDVAVICS 346
DB 59 TGPWLNEVKCKNESSLWCTARPMWCHSECHKELAAVNCI 100

Search Completed: August 20, 2002, 13:00:14
Job time: 148 sec

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1  NUMBER OF SEQUENCES: 17
2  CORRESPONDENCE ADDRESS:
3  ADDRESSEE: ROBINS & ASSOCIATES
4  STREET: 90 MIDDLEFIELD ROAD, SUITE 200
5  CITY: MENLO PARK
6  STATE: CALIFORNIA
7  COUNTRY: USA
8  ZIP: 94025
9  COMPUTER READABLE FORM:
10 MEDIUM TYPE: Floppy disk
11 COMPUTER: IBM PC compatible
12 OPERATING SYSTEM: PC-DOS/MS-DOS
13 SOFTWARE: Patent In Release #1.0, Version #1.30
14 CURRENT APPLICATION DATA:
15 APPLICATION NUMBER: US/09-034-916
16 FILING DATE: 04-MAR-1998
17 CLASSIFICATION: 536
18 PRIOR APPLICATION DATA:
19 APPLICATION NUMBER: US 60/039,956
20 FILING DATE: 06-MAR-1997
21 ATTORNEY/AGENT INFORMATION:
22 NAME: ROBINS, ROBERTA L.
23 REGISTRATION NUMBER: 34,208
24 REFERENCE/EX-REF NUMBER: 5998-0020
25 TELECOMMUNICATION INFORMATION:
26 TELEPHONE: (650) 325-7812
27 TELEFAX: (650) 325-7823
28 INFORMATION FOR SEQ ID NO: 15:
29 SEQUENCE CHARACTERISTICS:
30 LENGTH: 100 amino acids
31 TYPE: amino acid
32 STRANDEDNESS: single
33 TOPOLOGY: linear
34 MOLECULE TYPE: DNA (genomic)
35 US-09-034-916-15

Query Match 14.5%, Score 282; DB 3; Length 100;
Best Local Similarity 45.1%; Pred. No. 4,16-20;
Matches 46; Conservative 22; Mismatches 17; Gaps 2;

QY 245 RLVGRLNLSGSELEVLHKGVMWSVTHRWWEDEALQVYVCHLEDSHSESEPEHKLGYGPG 304
DB 1 RLVGRLNLSGSELEVLHKGVMWSVTHRWWEDEALQVYVCHLEDSHSESEPEHKLGYGPG 304

QY 305 VPRITDNYVRCSGEESQSFQCHRFWGFHDCIHQEDVAVICS 346
DB 59 TGPWLNEVKCKNESSLWCTARPMWCHSECHKELAAVNCI 100

RESULT 15
US-09-034-916-17
Sequence 17, Application US/09034916
Patent No. 6046314
GENERAL INFORMATION:
APPLICANT: GERE, JOHN A.
APPLICANT: SIADAK, ANTHONY W.
APPLICANT: ARUFFO, ALFANDRO A.
TITLE OF INVENTION: SCALPHIA: A NOVEL SCAVENGER RECEPTOR
TITLE OF INVENTION: CYSTEINE-RICH DOMAIN-CONTAINING POLYPEPTIDE AND RECOMBINANT
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROBINS & ASSOCIATES
STREET: 90 MIDDLEFIELD ROAD, SUITE 200
CITY: MENLO PARK
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

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GenCode version 4.5  
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OM protein - protein search, using sw model

Run on: August 20, 2002, 12:58:25 : Search time 17.6 seconds  
(without alignments)  
1694.135 MB total cell update size

Title: US-09-904-462A-148

Perfect score: 1947

Sequence: 1 MAILFSLLLAICTRPGFLAS.....RWCWRRCHRYGVAVYGV 47

Scoring table:

PIPSW62

Gapop 10.0 / Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

PIP-711\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Prod. No. is the number of results predicted by the search  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	754	29.7	1594	2	130549
2	726.5	27.4	2404	2	A59386
3	709	27.4	2387	2	232721
4	702	26.1	500	2	S56741
5	686	25.2	1249	2	138006
6	686	25.2	1151	2	148004
7	686	25.2	1151	2	148005
8	672.5	24.5	2152	2	T14893
9	663	24.1	1436	2	A14436
10	643	23.0	1036	2	T17405
11	639.5	22.8	2247	2	T15521
12	633	22.5	761	2	365759
13	582.5	20.9	1290	2	A57190
14	523	26.9	468	2	S26741
15	474.5	24.4	524	2	149100
16	459.5	23.6	918	2	364361
17	375.5	19.3	532	2	A12751
18	292.5	14.5	504	2	S56745
19	271.5	17.2	458	2	B11407
20	262.5	17.0	451	2	A98415
21	252	12.9	451	2	146852
22	251	12.9	451	2	S88276
23	249	12.8	454	2	A44467
24	217.5	12.7	518	2	A55840
25	235.5	12.1	494	1	A29079
26	231	11.9	501	1	S44536
27	223	11.5	577	2	A51202
28	216	11.1	585	2	A17161
29	198	10.2	495	1	A26396

RESULT 1  
130549  
headin - rabbit  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C:Date: 22 Oct 1999 #sequence\_revision 22 Oct 1999 #text\_date 21 Oct 1999  
C:Accession: 130549  
R:Rafiki, J.; Hikita, G.; Al-Awqati, O.  
J. Clin. Invest. '98, 2324-2331, 1996  
A:Title: headin, a new collecting duct protein involved in the in vitro plasticity of  
A:Reference number: Z20851; MUID:97096804  
A:Accession: T30549  
A:Status: preliminary; translated from OR/EMBL/DBD  
A:Molecule type: mRNA  
A:Residues: 1-1594 #TAX  
A:Lines reference: EMBL:AF01112, RIK:415548, F04410081, F0440242.1

ALIGNMENT

Query Match 38.7% Score 754; DB 2; Length 1594;

Best Local Similarity 40.4%; Prod. No. 4; se-49;

Matches 155; Conservative 43; Mismatches 120; Indels 66; Gaps 8;

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57 21 PSC AVLVSGVLRGPGVHVEVQVWTVTQWMTFRAVAVQFFVGAASQVPSGII 39
    III III I IIIIIII I IIIIIIIII I IIIIIII I IIIIIII I
58 48 FSGLELALASGSGQGVVIVLGGSKVTVCLQWLRHVAVVRGAGGDMAYSAI 107
    IIIIIIIII I IIIIIIIII I IIIIIIIII I IIIIIIIII I IIIIIIIII I
59 79 YETFAELRVLQSVSTHTFELATVFTT VVSGRPLAGASSTPPSSFSVPIR 146
    I IIIIIIIII I IIIIIIIII I IIIIIIIII I IIIIIIIII I IIIIIIIII I
60 108 F GQPGVGVLLDVSGSGQGVVLSVHRRGWSHGGHQLDAGVIGSDAMAMISPP 164
    I IIIIIIIII I IIIIIIIII I IIIIIIIII I IIIIIIIII I IIIIIIIII I
61 127 I IIIIIIIII I IIIIIIIII I IIIIIIIII I IIIIIIIII I IIIIIIIII I
62 165 THTVTVYHSHPHHTSGLELVVFTSGLELRLARSGVQGVTVVYGVSWIVHGW 204
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63 171 AAANVRLVTVAVVLPFQFQVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVV 228
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64 225 AAUVGVRGSGMAYCAP GSARVVGPGVIVLWVSSSGGVYVKSCHHGMESHNG 281
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65 229 NHDSTWVHCEHP IIIIIIIII IIIIIIIII IIIIIIIII IIIIIIIII 362
    IIIIIIIII I IIIIIIIII I IIIIIIIII I IIIIIIIII I IIIIIIIII I
66 282 GHQDAGVIGSDAMVPTTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPT 341
    IIIIIIIII I IIIIIIIII I IIIIIIIII I IIIIIIIII I IIIIIIIII I
67 293 VAVTVTVTVTVTVTVTVTVTVTVTVTVTVTVTVTVTVTVTVTVTVTVTV 322
    IIIIIIIII I IIIIIIIII I IIIIIIIII I IIIIIIIII I IIIIIIIII I
68 342 GSNVTVCLQWMTINDAVVVRGAGGDMAYSAIPQSAIP--PQGGVGVIVLWVSS 399
    IIIIIIIII I IIIIIIIII I IIIIIIIII I IIIIIIIII I IIIIIIIII I
69 423 EQGQHRFWGPHHTHOFEDVAVICS 346
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70 400 WSCVHRRGWSHGGHQLDAGVIG 424
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RESULT 2

A59386





[illegible][illegible]





[illegible]

Search completed: August 20, 2002, 13:00:49  
Job time: 134 sec



GenCore version 4.5  
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QM protein - protein search, using sw model

Run on: August 20, 2002, 12:55:16, Search time 15.6 seconds  
(without alignments)  
1001.169 Million cell updates/seq

Title: US-09-904-462A-148

Perfect score: 1947

Sequence: 1 MALLFSLHLAGTRGFLAS.....PPWGHDFGTHINAVI SV 447

Score and table: BLSDUM62

Gapop 10.0, Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	563	34.1	1436	1	WCL1_BOVIN
2	643	33.0	875	1	NETR_HUMAN
3	632	32.5	761	1	NPR_XMOUSE
4	523	26.9	568	1	CD6_HUMAN
5	480	24.7	753	1	LOL3_HUMAN
6	468.5	24.1	665	1	CD6_MOUSE
7	464.5	23.8	754	1	LOL3_MOUSE
8	453.5	23.3	774	1	LOL2_HUMAN
9	375.5	19.4	532	1	SPER_STRPU
10	269.5	13.1	520	1	MSRE_HUMAN
11	264.5	13.2	459	1	MSRE_MOUSE
12	262.5	13.0	451	1	MSRE_HUMAN
13	252	12.9	454	1	MSRE_RALIT
14	251	12.9	453	1	MSRE_BOVIN
15	247.5	12.7	518	1	MTG_MOUSE
16	245	12.6	483	1	MRCO_MOUSE
17	245.5	12.1	494	1	CD5_MOUSE
18	245.5	11.9	491	1	CD5_KAT
19	198	10.2	495	1	CD5_HUMAN
20	189	9.7	495	1	CD5_BOVIN
21	147	7.6	1113	1	CD1_MOUSE
22	145.5	7.5	5376	1	ZAN_MOUSE
23	138	7.1	469	1	PROP_HUMAN
24	132	7.0	455	1	TMS5_MOUSE
25	134.5	6.9	583	1	CEAL_HUMAN
26	133	6.7	1746	1	TENA_PIG
27	127.5	6.5	1584	1	BALL_HUMAN
28	125.5	6.4	4289	1	TENX_HUMAN
29	124.5	6.4	1042	1	CORT_HUMAN
30	121.5	6.2	4543	1	LRPI_CHICK
31	121	6.2	1709	1	BAR2_WHITE
32	121	6.2	4753	1	LRP_CALIL
33	120.5	6.2	4460	1	LRP_FAL

34 118 6.1 1115 1 GPCR\_TYMS  
35 117.5 6.0 1984 1 YL\_DROME  
36 117.5 6.0 3712 1 LMA\_DROME  
37 117 6.0 644 1 URM\_KAT  
38 115 5.9 860 1 ATSG\_HUMAN  
39 113 5.8 640 1 DROM\_HUMAN  
40 113 5.8 2201 1 TENA\_HUMAN  
41 112 5.2 3672 1 TMS2\_CALIL  
42 111.5 5.7 909 1 LRL\_XENLA  
43 111.5 5.7 2871 1 FBNI\_PIG  
44 111.5 5.7 4544 1 LRP\_HUMAN  
45 111 5.7 593 1 GRN\_HUMAN

## ALIGNMENTS

RESULT 1  
WCL1\_BOVIN STANDARD: PK1: 1436 AA.  
AC P30205;  
DT 01-APR-1993 (Rel. 25, Created)  
DT 01-APR-1993 (Rel. 25, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Antigen WCL1 precursor.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN 11  
RP SEQUENCE FROM N.A.  
RC TISSUE=Blood;  
RX MEDLINE=93056487; PubMed 141105;  
RA Wijngaard P.H.J., Metzelaar M.J., Machoud N.D., Morris W.L.,  
RA Clevers H.C.;  
RT "Molecular characterization of the WCL antigen expressed specifically  
on bovine CD4-CD8 gamma delta T lymphocytes".  
RL J. Immunol. 149:3273-3277(1992).  
CC 1- SUBCELLULAR LOCATION: Secreted.  
CC 1- SIMILARITY: CONTAINS 11 SECR DOMAINS.  
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This SWISS PROT entry is copyrighted. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk).  
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EMBL: X73723, 76637255.1;  
LR PIR: S19913; S19913;  
LR PIR: A46496; A46496;  
InterPro: IPR001190; SRCR.  
IR Pfam: PF00530; SRCR: 11.  
IR PRINTS: PR04258; SPERACTRPTK.  
IR SMART: SM00202; SR: 11.  
IR PROSITE: PS00420; SRCR: 1; 4.  
IR PROSITE: PS0267; SRCR: 2; 11.  
KW Antigen; Repeat; Glycoprotein; Signal.  
FT SIGNAL 1 25  
FT CHAIN 26 1436 ANTIGEN WCL1.1.  
FT DOMAIN 138 131  
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>> Strongyloides stercorarius.
>> NCBI TaxID 7608.
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>> SEQUENCE FROM N.A., AND SEQUENTIAL 477 489.
>> MEDLINE 98146152; PubMed 2529942;
>> Banquet L.J., Jordan J.E., Bellet K.A., Barbiers J.,
>> "Cloning of the mRNA for the protein that crosslinks to the cut
>> peptidic spectra.",
>> Proc. Natl. Acad. Sci. U.S.A. 86:2128-2132(1989).
>> [1] FUNCTION: RECEPTOR FOR THE EGF FIBRINOLYTIC.
>> [1] SUBCELLULAR LOCATION: Type II membrane protein.
>> [1] SIMILARITY: CONTAINS 4 SHC DOMAINS.
>>
>> This SWISS-Prot entry is copyrighted. It is produced through a collaboration
>> between the Swiss Institute of Bioinformatics and the EMBL outstation
>> at the European Bioinformatics Institute. There are no restrictions on its
>> use by non-profit institutions as long as its content is in no way
>> modified and this statement is not removed. Usage by and for commercial
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>> or send an email to license@isb.ch)
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>> EMBL: J04518; AAA0078.1;
>> PIR: A42751; A42751.
>> InterPro: IPR001193; ShcK.
>> Pfam: PF00540; ShcK_4.
>> PRINTS: PR06256; SHCAN127415.
>> SMART: SM00262; SR_4.
>> PROSITE: PS00424; ShcK_4.
>> PROSITE: PS00267; ShcK_2; 4.
>> Receptor: Transmembrane; cytoplasmic; Signal: Recept.
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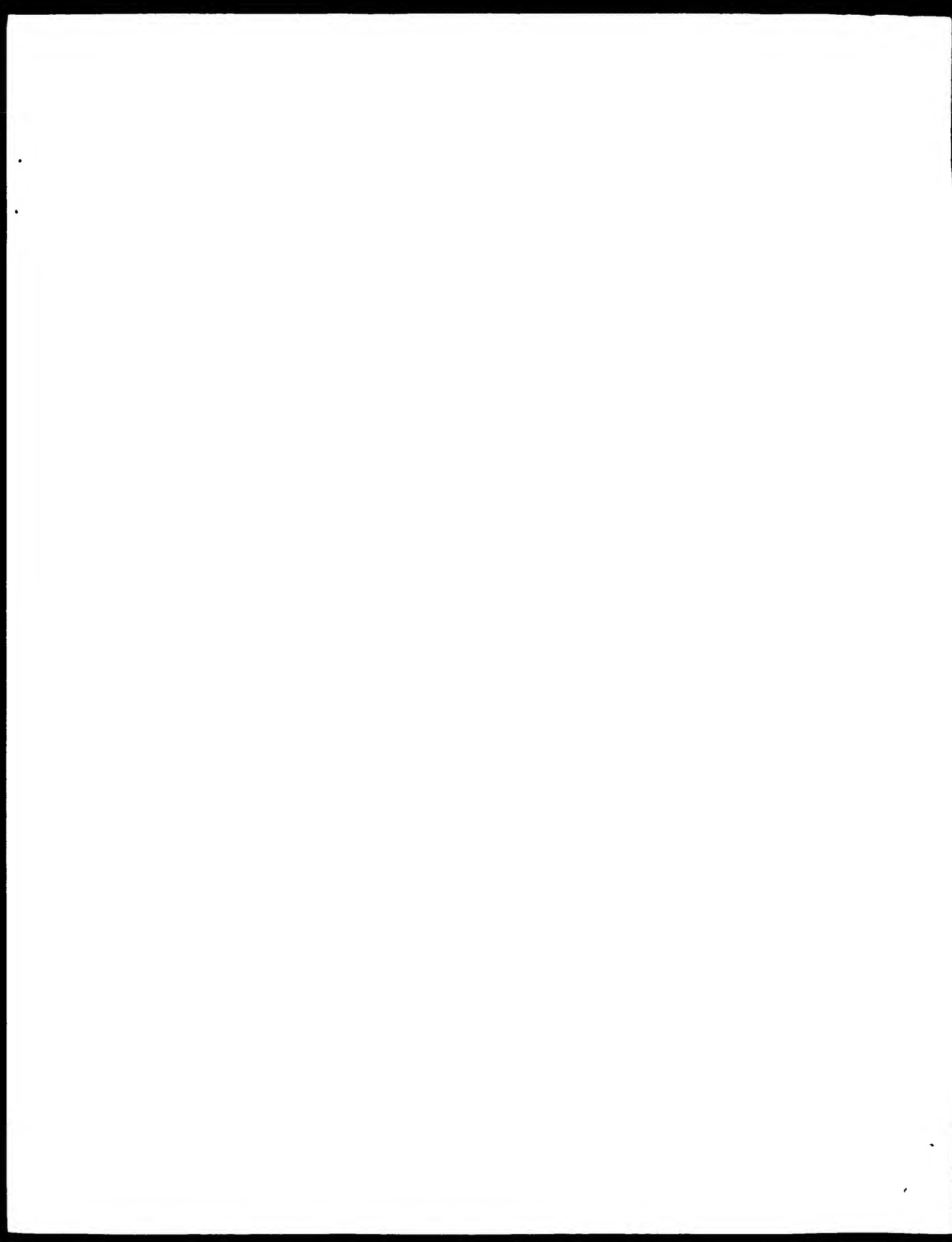












GenCore version 4.5  
Copyright (c) 1993 - 2000 Computer Mod.

OM protein - protein search, using SW model

Run on: August 20, 2002, 12:59:00, Search time 21.2 seconds  
(without alignments)  
2068,547 Matches, 53.1 of data/seq

Title: us-09-904-462a-148

Perfect score: 1447

Sequence: 1 MALLFSLILACTRCPLAS

Scoring table:

PROSUM62  
Gapop 10.0, Gapext 0.5

Searched: 562222 seqs, 17279429 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mice:\*
- 8: sp\_orqualelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_protein:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_virus:\*
- 16: sp\_bacterioph:\*
- 17: sp\_greep:\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

#### SUMMARIES

Result No	Score	Qty Match	Length	DB	ID	Description
1	1943	99.8	347	4	044866	044866 homo sapien
2	1341	68.9	352	11	045300	045300 mus musculus
3	1341	68.9	352	11	091W05	091W05 mus musculus
4	1339	68.9	352	11	091W07	091W07 mus musculus
5	1326	68.1	352	11	045301	045301 mus musculus
6	822	42.2	470	13	098T01	098T01 Gallus gall
7	754	38.7	1594	6	095218	095218 oryctolagus
8	747.5	37.9	2413	4	098J04	098J04 homo sapien
9	745.5	37.8	2412	4	095357	095357 homo sapien
10	744.5	37.7	2413	4	095304	095304 homo sapien
11	726.5	37.3	2403	4	090CM2	090CM2 homo sapien
12	725	37.3	2426	4	090CM3	090CM3 homo sapien
13	725	37.2	1785	4	098211	098211 homo sapien
14	722.5	37.1	1121	11	092M08	092M08 mus musculus
15	721	37.0	1785	4	0984V9	0984V9 homo sapien
16	709	36.4	1957	11	09JW09	09JW09 mus musculus

17	709	36.4	2084	11	095997	095997 mus musculus
18	705	36.2	600	4	Q28310	Q28310 bos taurus
19	691.5	35.5	1454	4	Q9NR16	Q9NR16 homo sapien
20	686	35.2	1116	4	Q07898	Q07898 homo sapien
21	686	35.2	1149	4	Q07901	Q07901 homo sapien
22	686	35.2	1151	4	Q07899	Q07899 homo sapien
23	686	35.2	1156	4	Q07900	Q07900 homo sapien
24	682.5	34.5	2153	7	Q57375	Q57375 strongyloce
25	661.5	33.3	369	6	Q29110	Q29110 sus scrofa
26	647.5	33.3	426	6	Q55J29	Q55J29 ovis aries
27	643	33.0	1046	5	Q97478	Q97478 strongyloce
28	636.5	32.8	2043	5	Q96943	Q96943 quedia cydo
29	636	32.7	749	5	Q9NC88	Q9NC88 strongyloce
30	635.5	32.5	1198	5	Q9NC87	Q9NC87 strongyloce
31	634	32.6	749	11	Q99J08	Q99J08 rattus norv
32	628	32.2	710	6	Q56J25	Q56J25 ovis aries
33	618	31.7	546	6	Q29111	Q29111 sus scrofa
34	618	31.7	973	5	Q9NC89	Q9NC89 strongyloce
35	617	31.7	1075	5	Q9NC90	Q9NC90 strongyloce
36	608	31.2	505	4	Q96180	Q96180 homo sapien
37	607	31.2	457	5	Q9NC91	Q9NC91 strongyloce
38	594.5	30.5	804	6	Q29113	Q29113 sus scrofa
39	582.5	29.9	1290	11	Q42927	Q42927 rattus norv
40	554	28.5	488	6	Q29112	Q29112 sus scrofa
41	517.5	26.6	264	6	Q91V20	Q91V20 oryctolagus
42	517.5	26.6	268	6	Q91V21	Q91V21 oryctolagus
43	517.5	26.6	277	6	Q91V21	Q91V21 oryctolagus
44	478	24.6	753	4	Q96R81	Q96R81 homo sapien
45	474.5	24.4	665	11	Q91W05	Q91W05 mus musculus

#### ALIGNMENTS

RESULT	ID	044866	PRELIMINARY	161	347 AA
AC	044866				
DT	01-JUN-1998	(TFMRLrel. 06, Created)			
DT	01-JUN-1998	(TFMRLrel. 06, Last sequence update)			
DT	01-JUN-2001	(TFMRLrel. 17, Last annotation update)			
DE	SP ALPHA (BA126D12.1)				
GN	CD56				
OS	Homo sapiens (human)				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
LA	NCBI_taxID=9606				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE: SPLEEN				
RA	Sabo J.A., Fisher P.A., Flint H.Z., Li X., Francke U., Aron A.				
RL	J. Biol. Chem. 0:0-0(1997).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RA	Miyazaki T., Yusa S.				
RT	*human CT-2 cDNA.*				
RL	Submitted (JUN 1997) to the EMBL/GenBank/CCDC databases.				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RA	Graham D.J.				
RL	J. Biol. Chem. 272:2737-2742 (1997)				
DR	EMBL: 082812; AAB91989.1; 1				
DR	EMBL: AF011429; AA01446.1; 1				
DR	EMBL: AL139409; CAC19458.1; 1				
DR	InterPro: IPR001190; SRCK				
DR	Print: PF00530; SRCK; 3				
DR	PRINTS: PR0258; SPERACTRPT				
DR	SMART: SM0002; SR; 3				
DR	PROSITE: PS00287; SRCK_2; 3				
DR	Receptor				
DR	SEQUENCE				
DR	347 AA; 38088 MW; 40ABBF08F9495183 CRC64;				







[illegible]









